Type: Poster Presentation

Final Abstract Number: 43.204
Session: Poster Session III
Date: Saturday, March 5, 2016
Time: 12:45-14:15
Room: Hall 3 (Posters & Exhibition)

Immature platelet fraction in Dengue cases

V.V. Kumar[1,*], S. Senthilkumaran[2], P. Thirumalaikolundusubramanain[3]

[1] *Chennai Medical College Hospital & Research Centre, Trichy, Tamil Nadu, India*
[2] *Erode Trust Hospital, Erode, India*
[3] *Chennai Medical College Hospital & Research Centre, Trichy, India*

Background: **Immature Platelet Fraction (IPF)** is an index of thrombopoiesis which quantitates reticulated platelets that have been recently released from the bone marrow.

Objectives: To find out the association between the status of immature platelet fraction (IPF) and the recovery of platelets in patients with dengue.

Methods & Materials: A prospective study was designed done to find out the association between the status of immature platelet fraction (**IPF**) and the recovery of platelets in **45 Dengue confirmed** (positive NS1 or IgM antibody dengue test) cases whose platelet count was less than one lakh/cumm with or without a downward trend. Platelet count and IPF were estimated using **Sysmex XE-2100 (Sysmex, Kobe, Japan)**. Complete blood count was recorded simultaneously and peripheral smears were studied in all these cases with a note for the presence of large platelets on smear. The cases were managed conservatively. The work was carried out after an approval from Institutional ethics committee. Data was analysed statistically.

Results: Among the recovery of platelets, **86.4%** showed recovery within 24hrs and the rest with 48 hrs after attaining peak IPF value. A single value IPF more than 10% was indicative of platelet recovery within 24-48 Hours. A positive correlation was observed among immature platelet fraction (IPF) level and the recovery of platelets in those patients with dengue.

Conclusion: IPF had a positive correlation with recovery of platelet counts in patients with dengue infections. Hence, Practitioners handling Dengue cases may be oriented to look for IPF, and consider it before referral or active intervention.

http://dx.doi.org/10.1016/j.ijid.2016.02.940

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Molecular detection and characterization of Sapovirus from hospitalized cases of acute gastroenteritis from western India

N. Lasure[1,*], V. Gopalkrishna[2]

[1] *National Institute of Virology, Pune, Maharashtra, India*
[2] *National Institute of Virology, Pune, India*

Background: Acute Gastroenteritis (AGE) accounts for 2.5-3 million deaths per year in children below 5 years of age. Among enteric viruses, Rotavirus is the leading cause of this diarrhoeal disease, followed by Norovirus, Adenovirus, Astrovirus and Aichivirus. Sapovirus (SaV), members of the *Caliciviridae* family are known to cause outbreaks and sporadic cases of AGE. SaVs are classified into 5 genogroups: GI-V, based on nucleotide variation in their capsid region. Among the 5 genogroups, GI, GII, GIV and GV are known to infect humans while GIII infect porcine and mink hosts. In India, studies on SaVs associated with AGE are available from northern, eastern and southern regions; however, no such data is available from Western India.

Methods & Materials: Stool samples of children ≤5 years of age (n=418), hospitalized for acute gastroenteritis; collected from Pune, Maharashtra, western India, between Jan 2009-Dec 2011 were included in the study. Detection and genotypic characterization of SaVs was carried out by amplification of the RdRp-Capsid junction region (~420bp). The amplicons were sequenced using ABI Prism ABI3730XL automated sequencer. Phylogenetic analysis of sequences was performed using MEGA 6 computational tool.

Results: SaVs were detected at an overall prevalence rate of 2.4% (10/418) in AGE cases. Co-infection with Astrovirus, Enterovirus and Adenovirus were observed in 3/10 cases (30%). SaV infections were observed in children ≤3 years of age, mostly in summer (60%) and monsoon (30%) with peak SaV activity reported in March (50%) . Severity assessment of AGE revealed mild (20%), moderate (40%) and severe (40%) infection in SaV positive cases. Phylogenetic analysis of study strains revealed the circulation of GGI (10%), GGII (50%) and GGV (40%) in the study region. GGI strain showed highest nucleotide identity with GGI strains from UK (100%), while GGII and GGV strains showed nucleotide identities ranging between 96.8%-99.6% and 99.2%-99.6% with their respective strains from UK, Thailand, Australia, Japan and USA.

Conclusion: The study reports circulation of GGV strains of SaV in AGE for the first time in India and also sheds light on the genotypic distribution of SaVs in Western India.

http://dx.doi.org/10.1016/j.ijid.2016.02.941